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Dated: September 23, 2004

Signature

(Monica L. Thomas)

Docket No.: HO-P01979US2
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:
Susan Lindquist , *et al.*

Application No.: 09/812,350

Filed: March 20, 2001

For: TRANSGENIC PLANTS CONTAINING HEAT
SHOCK PROTEIN



Group Art Unit: 1638

Examiner: Baum, Stuart F.

DECLARATION UNDER 37 CFR §1.132

Dear Sir:

I, Susan L. Lindquist, Ph.D., do hereby declare as follows:

1. I am a United States citizen residing at 85 Hilltop Road, Chestnut Hill, MA, 02467, USA.

2. I was an employee of the assignee of the above-referenced patent application at the time of filing, I am an inventor of said application, and I am familiar with the contents of said application.

3. Currently, I am a Professor of Biology at Massachusetts Institute of Technology and Director of Whitehead Institute for Biomedical Research in Cambridge, Massachusetts. I am skilled in the area of stress responses, plant molecular biology and transgenic plants.

4. I understand that the PTO examiner in charge of examining the referenced application is alleging that the references of Malik *et al.* (1999; "Malik") and Harndahl *et al.* (1998; "Harndahl") teach or suggest Hsp100 family amino acid sequences. This is incorrect for the reasons stated below.

5. I understand that the rejected claims are directed to Hsp100 family amino acid sequences having at least about 60% overall amino acid identity to SEQ ID NO:17. This means that the percentage of residues identical in an alignment between SEQ

ID NO:17 and a sequence in question is at least about 60%. This definition is known in the art, as supported in the attached printout of the definition from the website <http://alto.compbio.ucsf.edu/modbase/help.html>. Sequence identity may be further defined as the number of identical residues divided by the overlap, and is thus a fraction (percentage). This definition is also known in the art, as supported in the attached printout of the definition from the website http://www.niams.nih.gov/rcn/labbranch/labr/software/bsoft/bsoft_sequence.html.

I have reviewed sequence comparisons between the sequence of Malik (carrot Hsp17.7) with SEQ ID NO:17 and can state that there is a less than 20% identity between these sequences when compared overall. Even when gap parameters are changed, sequence identity is less than 28% over particular regions of the sequences. Sequence comparisons between SEQ ID NO:17 and Hsp17.7 using various alignment parameters are attached herewith.

6. Likewise, I have compared the sequence of Harndahl (Arabidopsis Hsp21) with SEQ ID NO:17 and determined that, again, there is less than a 20% sequence identity between these sequences when compared overall. Even when gap parameters are changed, sequence identity is less than 27% over particular regions of the sequences. These sequence comparisons are also attached herewith.

7. These sequence comparisons illustrate that the overall amino acid identity between the respective sequences and SEQ ID NO:17 is far below that of 60%. This is to be expected, given that the vast difference in size (17.7 kD for carrot Hsp17.7 and 21kD for Arabidopsis Hsp21 versus approximately 100 kD for Arabidopsis Hsp101 of SEQ ID NO:17) indicates that these are in fact not in the Hsp100 family of amino acid sequences. Furthermore, the small Hsps at the time of this invention were broadly recognized in the art as having distinct functions and evolutionary history from the Hsp100s.

8. I hereby declare that all statements made herein on my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: Sept 20, 2004

Susan Lindquist
Susan L. Lindquist, Ph.D.